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DB=USPT,PGPB,JPAB,EPAB,DWPI,TDBD; PLUR=YES;
OP=AND

L1	(campylobacter or cjejuni or jejuni or coli or lari)	68952	L1
L2	(rec or reca or rec-a or recombinase)	14359	L2
L3	L2 same l1	1693	L3
L4	L3 not coli	1	L4
L5	L3 same campylobacter	8	L5
L6	L3 and jejuni	45	L6
L7	L6 not l4 not l5	38	L7

END OF SEARCH HISTORY

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DATE: Wednesday, March 26, 2003

<u>Set Name</u>	<u>Query</u>	<u>Hit</u> <u>Count</u>	<u>Set</u> <u>Name</u> result set
side by side			
<i>DB=USPT,PGPB,JPAB,EPAB,DWPI,TDBD; PLUR=YES; OP=AND</i>			
L1	(campylobacter or cjejuni or jejuni or coli or lari)	68952	L1
L2	(rec or reca or rec-a or recombinase)	14359	L2
L3	L2 same l1	1693	L3
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L5	L3 same campylobacter	8	L5
L6	L3 and jejuni	45	L6
L7	L6 not l4 not l5	38	L7
L8	(campylobacter or cjejuni or jejuni or lari)	2864	L8
L9	L8 same l2	8	L9

END OF SEARCH HISTORY

Infect. Immun., 02 1994, 426-432, Vol 62, No. 2
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Development and characterization of *recA* mutants of *Campylobacter* *jejuni* for inclusion in attenuated vaccines

P Guerry, PM Pope, DH Burr, J Leifer, SW Joseph and AL Bourgeois

Enterics Program, Naval Medical Research Institute, Bethesda, Maryland 20814.

Isogenic *recA* mutants of *Campylobacter jejuni* have been constructed for evaluation of their usefulness in attenuated vaccines against this major worldwide cause of diarrhea. The *recA*⁺ gene of *C. jejuni* 81-176 was cloned by using degenerate primers to conserved regions of other RecA proteins in a PCR. The *C. jejuni recA*⁺ gene encodes a predicted protein with an M(r) of 37,012 with high sequence similarity to other RecA proteins. The termination codon of the *recA*⁺ gene overlaps with the initiation codon of another open reading frame which encodes a predicted protein which has > 50% identity with the N terminus of the *Escherichia coli* enolase protein. A kanamycin resistance gene was inserted into the cloned *recA*⁺ gene in *E. coli* and returned to *C. jejuni* VC83 by natural transformation, resulting in allelic replacement of the wild-type *recA* gene. The resulting VC83 *recA* mutant displayed increased sensitivity to UV light and a defect in generalized recombination as determined by natural transformation frequencies. The mutated *recA* gene was

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amplified from VC83 *recA* by PCR, and the product was used to transfer the mutation by natural transformation into *C. jejuni* 81-176 and 81-116, resulting in isogenic *recA* mutants with phenotypes similar to VC83 *recA*. After oral feeding, strain 81-176 *recA* colonized rabbits at levels comparable to wild-type 81-176 and was capable of eliciting the same degree of protection as wild-type 81-176 against subsequent homologous challenge in the RITARD (removable intestinal tie adult rabbit diarrhea) model.

This article has been cited by other articles:

- Sander, P., Papavinasasundaram, K. G., Dick, T., Stavropoulos, E., Ellrott, K., Springer, B., Colston, M. J., Bottger, E. C. (2001). *Mycobacterium bovis* BCG *recA* Deletion Mutant Shows Increased Susceptibility to DNA-Damaging Agents but Wild-Type Survival in a Mouse Infection Model. *Infect. Immun.* 69: 3562-3568 [[Abstract](#)] [[Full Text](#)]
- Bacon, D. J., Alm, R. A., Burr, D. H., Hu, L., Kopecko, D. J., Ewing, C. P., Trust, T. J., Guerry, P. (2000). Involvement of a Plasmid in Virulence of *Campylobacter jejuni* 81-176. *Infect. Immun.* 68: 4384-4390 [[Abstract](#)] [[Full Text](#)]
- Wösten, M. M. S. M., Boeve, M., Koot, M. G. A., van Nuenen, A. C., van der Zeijst, B. A. M. (1998). Identification of *Campylobacter jejuni* Promoter Sequences. *J. Bacteriol.* 180: 594-599 [[Abstract](#)] [[Full Text](#)]

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[J. Virol.](#)

[Eukaryot. Cell](#)

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ANNEX V

Strategy for the selection of the amplification primers specific
for the genus *Streptococcus* from the *recA* gene.

	181	220.....301	340
<i>tella pertussis</i>	CTCGAGATCA	CCGACGCGCT GGTGCGCTCG GGCTCGGTTCG....CTGCAGGCC	GCCTGATGAG CCAGGCGCTG CGCAAGCTGA
<i>lobacter jejuni</i>	TTAGAAATTG	TAGAACTAT AGCAAGAAGT GGCGCAGTAG....CTTCAAGCAA	GACTTATGTC TCAAGCTCTA AGAAACTTA
<i>idia trachomatis</i>	TTGAGTATTG	CAGAGCTCTT AGCGCGTTCT GGAGCTGTCG....TTGCAAGCTC	GCATGATGTC GCAGGCTCTA CGCAAATTAA
<i>obacter agglomerans</i>	CTGGAAATCT	GTGATGCGCT GACCCGTTCA GGCGCCGTTG....CTCGCAGCTC	GTATGATGAG CCAGGCGATG CGTAAGCTTG
<i>richia coli</i>	CTGGAAATCT	GTGACGCCCT GGCGCGTTCT GGCGCAGTAG....CTGCGGCAC	GTATGATGAG CCAGGCGATG CGTAAGCTTG
<i>philus influenzae</i>	GCGAACAGAA	GATAGAATT TTAATGCATT ACCGCTGTG....AATTGACCT	GTGAGTTTAC GCAAAGCTTG AGACATTAAA
<i>occus lactis</i>	CTTCAAAATG	CTGAAAAATT GATTACTTCT GGAGCGGTTG....CTACAAGCAC	GTATGATGTC ACAAGCCATG CGTAACTTG
<i>eria gonorrhoeae</i>	TTGGAAATCT	GCGACGCGCT CGTCCGTTCC GGCGGCATAG....CTGCAGGCGC	GCCTGATGAG TCAGGCTTTG CGCAAATGA
<i>us mirabilis</i>	CTGGAAATTT	GTGATGCATT ATCTCGCTCT GGTGCGGTTCG....TTAGCCGCAC	GTATGATGAG CCAAGCTATG CGTAACTAG
<i>us vulgaris</i>	CTGGAGATCT	GTGATGCACT CACGCGCTCT GGCGCTGTTG....CTTGCAGCAC	GTATGATGAG CCAGGCTATG CGTAACTGG
<i>omonas aeruginosa</i>	CTGGAAATCA	CCGACATGCT GGTGCGCTCC AACGCGGTTCG....CTGCAGGCAC	GCCTGATGTC CCAGGCGCTG CGCAAGATCA
<i>omonas cepacia</i>	CTCGAAATCA	CCGATGCGCT GGTGCGCTCG GGCTCGATCG....CTGCAGGCC	GCCTGATGTC GCAGGCGCTG CGCAAGCTGA
<i>omonas putida</i>	CTGGAAATCA	CCGACATGCT GGTGCGTTCC AACGCGGTTCG....CTGCAGGCTC	GCCTGATGTC CCAGGCGCTG CGCAAAATCA
<i>tia marcescens</i>	CTGGAAATCT	GTGATGCGCT GACCCGCTCC GGCGCGGTTG....CTGGCGGCGC	GCATGATGAG CCAGGCGATG CGTAAGCTGG
<i>ylcococcus aureus</i>	CTTGAAATCG	CCGAAGCATT TGTTAGAAGT GGTGCAATTG....TTACAAGCTC	GTTTAATGTC ACAAGCGTTA CGTAACTTT
<i>ococcus gordonii</i>	TTAGAAATTG	CAGGAAATT GATTGACTCT GGGGCAATTG.....
<i>ococcus mutans</i>	CTTGAAATTG	CAGGAAATT GATTGATTCT GGCGCTGTTG....TTACAAGCAC	GCATGATGAG TCAAGCGATG CGTAAATTAT
<i>ococcus pneumoniae</i>	CTTGAGATTG	CGGAAATT GATTGACTCA GGTGCAATTG....TTGCAGGCTC	GTATGATGAG CCAGGCCATG CGTAACTTG
<i>ococcus pyopenes</i>	CTTGAAATTG	CAGGTAAATT GATTGATTCT GGTGCGGTTG....TTGCAAGCAC	GTATGATGAG TCAGGCCATG CGTAAATTAT
<i>ococcus salivarius</i>	CTCGAAATTG	CAGCTAAGCT GATTGACTCT GGTGCAATTG....CTTCAAGCGC	GTATGATGAG TCAAGCCATG CGTAACTTT
<i>cholerae</i>	CTGGAAATTT	GTGATGCACT GGCTCGCTCT GGTGCTGTGG....CTGCAAGCGC	GTATGTTGTC GCAAGCAATG CGTAACTGA
<i>ia pestis</i>	CTGGAAATTT	GTGATGCGCT GACTCGCTCT GGTGCGGTTG....CTTGCCGCGC	GTATGATGAG CCAGGCTATG CGTAAGCTGG
sequences for the treptococcus species:	G G T GC GAAATTG CAGGAAATT GATTGA		C G G ATGATGAG TCAAGCCATG CGTAA

WEST**End of Result Set**

Generate Collection

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L7: Entry 38 of 38

File: USPT

Jun 21, 1994

DOCUMENT-IDENTIFIER: US 5322784 A

TITLE: Method and materials for introducing DNA into *Prevotella ruminicola*Drawing Description Text (8):

FIGS. 6A and 6B show the deduced amino acid sequence of TetQ aligned with representatives of TetO (*Campylobacter jejuni*) and TetM (*Streptococcus faecalis*). The consensus of the sequenced ribosomal protection Tc.sup.r genes is displayed below these sequences. Upper case denotes conservation among the ribosome protection Tc.sup.r proteins. The four barred regions are regions of conservation in GTP-binding proteins [Halliday, J. Nucleotide Prot. Phosphoryl. Res., 9:435-448 (1984)]. Positions marked (*) were found to be involved directly in GTP binding and are invariant in all GTP-binding proteins [Jurnak, Science. 230:32-36 (1985)].

Drawing Description Text (9):

FIGS. 7A and 7B show the upstream sequence of tetQ. The endpoints of the pNFD13-2 deletions shown in FIG. 4 are indicated by numbers above the sequence. Only the last three characters of the deletion designations are given. The first letter in parenthesis at each deletion denotes Tc.sup.r expression in *E. coli* (R=resistant; I=intermediate; S=sensitive). The letter following the slash denotes Tc.sup.r expression in *Bacteroides*. The *E. coli* consensus -35 and -10 sequences are indicated by lines above the tetQ sequence. Below the tetQ upstream sequence is shown the upstream consensus of the tetM sequences from *Staphylococcus aureus*, *Streptococcus faecalis*, and *Ureaplasma urealyticum* and the tetO sequences from *Campylobacter coli*, *Campylobacter jejuni*, and *Streptococcus mutans*. Upper case letters denote bases that are conserved in all tetM and tetO sequences. Lower case letters denote bases that are not conserved in all cases, but are the consensus for that position. If data were not available for all six upstream sequences at a position, a lower case letter was used at that position.

Detailed Description Text (121):

Previously sequenced ribosome protection Tc.sup.r genes were remarkable for their sequence similarity (Table 4). For instance, the TetO found in *Campylobacter jejuni* shared 98.1% intraclass amino acid identity with the TetO found in *Streptococcus mutans*. The *C. jejuni* TetO shared 75.1-76.8% interclass amino acid identity with the TetM's found in *Staphylococcus*, *Streptococcus*, and *Ureaplasma*. Genes that are similar enough to cross-hybridize with tetM and tetO on Southern blots have been found in *Clostridium*, *Eikenella*, *Fusobacterium*, *Gardnerella*, *Hemophilus*, *Kingella*, *Mycoplasma*, *Neisseria*, and *Veillonella* [Salyers, et al., Mol. Microbiol., 4:151-156 (1989)].

Detailed Description Paragraph Table (2):


TABLE 2 _____ Strains Used In Connection With Sequencing Of
 Tc.sup.r Strain or Relevant Plasmid Phenotype _____ E. coli
 strains DH5.alpha. RecA .DELTA.(argF-lacA)U169 .theta.80dlac.DELTA.M15 LCD44 RecA MetE Tc.sup.s
 derivative of RK5173. Bacteroides strains B. thetaiotaomicron 5482 BT4001 Tc.sup.s Em.sup.s ; Spontaneous
 Rif.sup.r derivative of B. thetaiotaomicron 5482 BT4002 Tc.sup.r BT4004 Tc.sup.r BT4007 Tc.sup.r Em.sup.r
 BT4008 Tc.sup.r Em.sup.r 2808 Tc.sup.r B. uniformis BU1001 Tc.sup.s ; Rif.sup.r derivative of B. uniformis
 0061 C7-17 Tc.sup.r 3537 Tc.sup.r T1-1 Tc.sup.r B. distasonas 4243 Tc.sup.s C30-45 Tc.sup.r 6308 Tc.sup.r B.
 caccae 3452A Tc.sup.s 8608 Tc.sup.r B. fragilis AK87 Tc.sup.r
 _____ .sup.a Resistance phenotype expressed in E. coli is
 indicated in parenthesis.

Detailed Description Paragraph Table (3):

TABLE 3 _____ GenBank Access Codes For Sequences Source
 Gene GenBank GenBank organism product Locus Access. _____
 Staphylococcus aureus TetM Statetm M21136 Streptococcus faecalis TetM Str1545tr X04388 Ureaplasma
 urealyticum TetM X06901 X06901 Campylobacter jejuni TetO Cajtrccra M18896 Streptococcus mutans TetO
 Stateosm M20925 Escherichia coli EF-Tu Ecotgtufb J01717 EF-G Ecostra X00415 Micrococcus luteus EF-Tu
 M17788 M17788 EF-G M17788 M17788 Spirulina platensis EF-Tu X15646 X15646 EF-G X15646 X15646
 Thermus thermophilus EF-Tu Tthtuf1 X05977 EF-G X16278 X16278 Thermotoga maritima EF-Tu Tmoeftu
 M27479 Euglena gracilis EF-Tu Egrcpeftu X00044 chloroplast Methanococcus vannielii EF-1 Mvatuf X05698
 EF-2 Mvafus X12384 Saccharomyces EF-1.alpha. Yscefla X00779 cerevisiae Mucor racemonsus EF-1.alpha.
 Mratefla J02605 Dictyostelium EF-2 Ddief2 M26017 discoideum Drosophila melanogaster EF-2 X15805
 X15805 Xenopus laevis EF-1.alpha. Xelefla1 M5697 Mesocricetus sp. EF-2 Hamef2 M13708 Mus musculus
 EF-1.alpha. M22432 M22432 Rattus norvegicus EF-2 Ratef2r Y07504 Homo sapiens EF-1.alpha. Humef1a
 X03558 EF-2 Humef2ab M30456 _____

Detailed Description Paragraph Table (4):

TABLE 4 _____ Percent amino acid similarity and percent amino
 acid identity between deduced peptide sequences of ribosome protection tetracycline resistance genes
 percent similarity 1 2 3 4 5 6 _____ 1. S. aureus TetM -- 95.3
 98.1 85.3 85.9 62.5 2. S. pneumoniae TetM 92.2 -- 96.7 85.7 86.1 61.1 3. U. urealyticum TetM 96.6 95.0 --
 85.7 86.3 62.5 4. C. jejuni TetO 75.1 76.8 76.0 -- 98.4 60.5 5. S. mutans TetO 75.6 76.9 76.4 98.1 -- 60.8 6.
 B. thetaiotaomicron 41.2 41.0 41.2 41.0 41.0 -- TetQ percent identity
 _____ ##STR2##

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Search for

Search in Swiss-Prot and TrEMBL for: recombinase campylobacter

Swiss-Prot Release 41.0 of 05-Mar-2003

TrEMBL Release 23.0 of 04-Mar-2003

-
- Number of sequences found in Swiss-Prot₍₅₎ and TrEMBL₍₂₉₎: 34
 - Note that the selected sequences can be saved to a file to be later retrieved; to do so, go to the bottom of this page.
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-

Search in Swiss-Prot: There are matches to 5 out of 122564 entries

RECA_CAMFE (O30884)

RecA protein (Recombinase A). {GENE: RECA} - Campylobacter fetus

RECA_CAMJE (P42440)

RecA protein (Recombinase A). {GENE: RECA OR CJ1673C} -
Campylobacter jejuni

RECA_CAMLA (Q93R37)

RecA protein (Recombinase A). {GENE: RECA} - Campylobacter lari
RECA_HELPJ (Q9ZMS7)

RecA protein (Recombinase A). {GENE: RECA OR JHP0141} - Helicobacter pylori J99 (Campylobacter pylori J99)

RECA_HELPY (P42445)

RecA protein (Recombinase A). {GENE: RECA OR HP0153} - Helicobacter pylori (Campylobacter pylori)

Search in TrEMBL: There are matches to 29 out of 830524 entries

O25386

Integrase/recombinase (XERC) {GENE:HP0675} - Helicobacter pylori (Campylobacter pylori)

O25643

Integrase/recombinase (XERD) {GENE:HP0995} - Helicobacter pylori (Campylobacter pylori)

O25653

Site-specific recombinase {GENE:HP1009} - Helicobacter pylori (Campylobacter pylori)

Q8VLF3

RecA protein (Recombinase A) {GENE:RECA} - Campylobacter lari

Q8VLM8

Recombinase RecA (RecA protein) (Recombinase A) {GENE:RECA} - Helicobacter pylori (Campylobacter pylori)

Q93CN0

Recombinase A (RecA protein) (Fragment) {GENE:RECA} - Helicobacter pylori (Campylobacter pylori)

Q9ETW3

RecA protein (Recombinase A) (Fragment) {GENE:RECA} - Helicobacter pylori (Campylobacter pylori)

Q9ETW4

RecA protein (Recombinase A) (Fragment) {GENE:RECA} - Helicobacter

pylori (*Campylobacter pylori*)

Q9ETY4

RecA protein (Recombinase A) (Fragment) {GENE:RECA} - *Helicobacter pylori* (*Campylobacter pylori*)

Q9ETY5

RecA protein (Recombinase A) (Fragment) {GENE:RECA} - *Helicobacter pylori* (*Campylobacter pylori*)

Q9EU00

RecA protein (Recombinase A) (Fragment) {GENE:RECA} - *Helicobacter pylori* (*Campylobacter pylori*)

Q9EU05

RecA protein (Recombinase A) (Fragment) {GENE:RECA} - *Helicobacter pylori* (*Campylobacter pylori*)

Q9EU06

RecA protein (Recombinase A) (Fragment) {GENE:RECA} - *Helicobacter pylori* (*Campylobacter pylori*)

Q9EU56

RecA protein (Recombinase A) (Fragment) {GENE:RECA} - *Helicobacter pylori* (*Campylobacter pylori*)

Q9EU57

RecA protein (Recombinase A) (Fragment) {GENE:RECA} - *Helicobacter pylori* (*Campylobacter pylori*)

Q9EU77

RecA protein (Recombinase A) (Fragment) {GENE:RECA} - *Helicobacter pylori* (*Campylobacter pylori*)

Q9EU90

RecA protein (Recombinase A) (Fragment) {GENE:RECA} - *Helicobacter pylori* (*Campylobacter pylori*)

Q9F4P3

RecA protein (Recombinase A) (Fragment) {GENE:RECA} - *Helicobacter pylori* (*Campylobacter pylori*)

Q9F4P4

RecA protein (Recombinase A) (Fragment) {GENE:RECA} - *Helicobacter pylori* (*Campylobacter pylori*)

Q9F4P5

RecA protein (Recombinase A) (Fragment) {GENE:RECA} - Helicobacter pylori (Campylobacter pylori)

Q9F4P6

RecA protein (Recombinase A) (Fragment) {GENE:RECA} - Helicobacter pylori (Campylobacter pylori)

Q9F4P7

RecA protein (Recombinase A) (Fragment) {GENE:RECA} - Helicobacter pylori (Campylobacter pylori)

Q9F4P8

RecA protein (Recombinase A) (Fragment) {GENE:RECA} - Helicobacter pylori (Campylobacter pylori)

Q9F4P9

RecA protein (Recombinase A) (Fragment) {GENE:RECA} - Helicobacter pylori (Campylobacter pylori)

Q9F4Q0

RecA protein (Recombinase A) (Fragment) {GENE:RECA} - Helicobacter pylori (Campylobacter pylori)

Q9PP60

DNA recombinase {GENE:XERD OR CJ0863C} - Campylobacter jejuni

Q9ZKI4

Integrase/recombinase (XERCD family) {GENE:JHP0951} - Helicobacter pylori J99 (Campylobacter pylori J99)

Q9ZKJ4

Integrase/recombinase (XERCD family) {GENE:JHP0941} - Helicobacter pylori J99 (Campylobacter pylori J99)

Q9ZLG3

Integrase-recombinase protein (XERCD family) {GENE:JHP0617} - Helicobacter pylori J99 (Campylobacter pylori J99)

in Swiss-Prot/TrEMBL by AC, ID,
description, gene name, organism
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Entry name	Q8VLF3
Primary accession number	Q8VLF3
Secondary accession numbers	None
Entered in TrEMBL in	Release 20, March 2002
Sequence was last modified in	Release 20, March 2002
Annotations were last modified in	Release 22, October 2002

Name and origin of the protein

Protein name	RecA protein
Synonym	Recombinase A
Gene name	RECA
From	<u>Campylobacter lari</u> [TaxID: <u>201</u>]
Taxonomy	<u>Bacteria</u> ; <u>Proteobacteria</u> ; <u>Epsilonproteobacteria</u> ; <u>Campylobacterales</u> ; <u>Campylobacteraceae</u> ; <u>Campylobacter</u> .

References

- [1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=CF89-14;
Honda M., Matsushita S., Matsui T., Murayama O., Miller B.C., Moore J.E.,
Matsuda M.;
 "Cloning and sequence analysis of the recA gene of urease-positive thermophilic Campylobacter."
 Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
- [2] SEQUENCE FROM NUCLEIC ACID.
STRAIN=CF89-12;
Honda M., Matsushita S., Matsui T., Murayama O., Miller B.C., Moore J.E.,
Matsuda M.;
 "Cloning and sequence analysis of the recA gene of urease-positive thermophilic Campylobacter."
 Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

Comments

- **FUNCTION:** Can catalyze the hydrolysis of ATP in the presence of

single-stranded DNA, the ATP-dependent uptake of single-stranded DNA by duplex DNA, and the ATP-dependent hybridization of homologous single-stranded DNAs. It interacts with *lexA* causing its activation and leading to its autocatalytic cleavage (*By similarity*).

- **SIMILARITY:** BELONGS TO THE RECA FAMILY.

Cross-references

EMBL	AB076251; [EMBL / GenBank / DDBJ] BAB79454.1; -. [CoDingSequence] AB074463; [EMBL / GenBank / DDBJ] BAB72097.1; -. [CoDingSequence]
InterPro	IPR003593; AAA_ATPase. IPR001553; RecA. Graphical view of domain structure.
Pfam	PF00154; recA; 1.
PRINTS	PR00142; RECA.
ProDom	PD000229; RecA; 1. [Domain structure / List of seq. sharing at least 1 domain].
SMART	SM00382; AAA; 1.
PROSITE	PS00321; RECA_1; 1. PS50162; RECA_2; 1. PS50163; RECA_3; 1.
ProtoMap	Q8VLF3.
PRESAGE	Q8VLF3.
ModBase	Q8VLF3.
SWISS-2DPAGE	Get region on 2D PAGE.

Keywords

ATP-binding; DNA damage; DNA recombination; DNA repair; DNA-binding; SOS response.

Features

None

Sequence information

Length: 344 AA	Molecular weight: 37200 Da	CRC64: 6A3A3F83CBEBB35B [This is a checksum on the sequence]
--------------------------	--------------------------------------	--

10	20	30	40	50	60
MDDNKRKSLD	AALKSLDKTF	GKGTILRLGD	KEVEKIDSIP	TGSVGLDLAL	GIGGVPKGRI
70	80	90	100	110	120
IEIYGPESSG	KTTTLTHIIA	ECQKKGVCVCA	FIDAEHALDV	RYAKNLGVDI	ENLYISQPDF
130	140	150	160	170	180
GEQALEIVET	IARSGAIDLI	VVDSVAALTP	KAEIEGDMGD	QHVGLQARLM	SQALRELTGI
190	200	210	220	230	240
VHKMNTTVIF	INQIRMRIIM	MGYGTPEITTT	GGNALKFYAS	VRLDVRKTAT	LKQNDPEIGN
250	260	270	280	290	300
RVKVKVAKNK	VAPPFKQAEF	DVMFGEGVSR	EGELIDYGVK	LDIIDKSGAW	FSYKASKLGQ
310	320	330	340		
GRENAKFLK	ENPAIADEIT	QAIONSIGID	SMILGAKEDD	EGDE	

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General information about the entry

Entry name	RECA_CAMLA
Primary accession number	Q93R37
Secondary accession number	Q93R36
Entered in Swiss-Prot in	Release 41, February 2003
Sequence was last modified in	Release 41, February 2003
Annotations were last modified in	Release 41, February 2003

Name and origin of the protein

Protein name	RecA protein
Synonym	Recombinase A
Gene name	RECA
From	<u>Campylobacter lari</u> [TaxID: 201]
Taxonomy	<u>Bacteria</u> ; <u>Proteobacteria</u> ; <u>Epsilonproteobacteria</u> ; <u>Campylobacterales</u> ; <u>Campylobacteraceae</u> ; <u>Campylobacter</u> .

References

- [1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=JCM 2530;
Honda M., Matsushita S., Murayama O., Millar B.C., Moore J.E., Matsuda M.;
"Cloning and sequence analysis of the recA gene of *Campylobacter lari* JCM2530.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
- [2] SEQUENCE FROM NUCLEIC ACID.
STRAIN=NCTC 12894;
Matsuda M., Honda M., Matsushita S., Matsui T., Murayama O., Millar B.C., Moore J.E.;
"Cloning and sequence analysis of the recA gene of urease-positive thermophilic *Campylobacter*.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

Comments

- **FUNCTION:** Can catalyze the hydrolysis of ATP in the presence of

single-stranded DNA, The ATP-dependent uptake of single-stranded DNA by duplex DNA, and the ATP-dependent hybridization of homologous single-stranded DNAs. It interacts with *lexA* causing its activation and leading to its autocatalytic cleavage (*By similarity*).

- **SUBCELLULAR LOCATION:** Cytoplasmic (*By similarity*).
- **SIMILARITY:** BELONGS TO THE RECA FAMILY.

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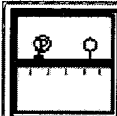
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Cross-references

EMBL	AB067767;	[EMBL / GenBank / DDBJ]
	BAB62716.1; -.	[CoDingSequence]
	AB067768;	[EMBL / GenBank / DDBJ]
	BAB62717.1; -.	[CoDingSequence]
HAMAP	MF_00268; -; 1.	
InterPro	IPR003593; AAA_ATPase.	
	IPR001553; RecA.	
	Graphical view of domain structure.	
Pfam	PF00154; recA; 1.	
PRINTS	PR00142; RECA.	
ProDom	PD000229; RecA; 1.	
	[Domain structure / List of seq. sharing at least 1 domain] .	
SMART	SM00382; AAA; 1.	
PROSITE	PS00321; RECA_1; 1.	
	PS50162; RECA_2; 1.	
	PS50163; RECA_3; 1.	
BLOCKS	Q93R37 .	
ProtoNet	Q93R37 .	
ProtoMap	Q93R37 .	
PRESAGE	Q93R37 .	
DIP	Q93R37 .	

ModBase Q93R37.

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KeywordsDNA damage; DNA recombination; SOS response; ATP-binding;
DNA-binding.**Features**Feature table viewer

Key	From	To	Length	Description
NP_BIND	65	72	8	ATP (BY SIMILARITY) .
VARIANT	101	101		K -> R (IN STRAIN NCTC 12894) .
VARIANT	105	105		D -> N (IN STRAIN NCTC 12894) .
VARIANT	176	176		E -> K (IN STRAIN NCTC 12894) .
VARIANT	219	219		S -> A (IN STRAIN NCTC 12894) .
VARIANT	342	343		GD -> EGE (IN STRAIN NCTC 12894) .

Sequence information

Length: 344 AA Molecular weight: 37161 Da CRC64: 5CF9C3AD5E045C52 [This is a checksum on the sequence]

```

      10      20      30      40      50      60
MDDNKRKSLD AALKSLDKTF GKG TILRLGD KEVEKIDSIP TGSVGLDLAL GIGGVPKGRI

      70      80      90     100     110     120
IEIYGPESSG KTTTLTHIIA ECQKKGGVCA FIDAEHALDV KYAKDLGVDT ENLYISQPDF

     130     140     150     160     170     180
GEQALEIVET IARSGAIDLI VVDSVAALTP KAEIEGDMGD QHVGLQARLM SQALRELTGI

     190     200     210     220     230     240
VHKMNTTVIF INQIRMKIGM MGYGTPETTT GGNALKFYSS VRLDVRKTAT LKQNDPEIGN

     250     260     270     280     290     300
RVKVKVAKNK VAPPFKQAEF DVMFGEGVSR EGELIDYGVK LDIIDKSGAW FSYKASKLGQ

     310     320     330     340
GRENAKAFLK ENPAIADEIT QAIQNSIGID SMILGAKEDD EGDE

```

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[PeptideMass](#), [PeptideCutter](#),
[Dotlet](#) (Java)



[ScanProsite](#),
[MotifScan](#)



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General information about the entry

Entry name	RECA_CAMFE
Primary accession number	O30884
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 36, July 1998
Sequence was last modified in	Release 36, July 1998
Annotations were last modified in	Release 41, February 2003

Name and origin of the protein

Protein name	RecA protein
Synonym	Recombinase A
Gene name	RECA
From	<u>Campylobacter fetus</u> [TaxID: <u>196</u>]
Taxonomy	<u>Bacteria</u> ; <u>Proteobacteria</u> ; <u>Epsilonproteobacteria</u> ; <u>Campylobacterales</u> ; <u>Campylobacteraceae</u> ; <u>Campylobacter</u> .

References

- [1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=23D;
 MEDLINE=98053868; PubMed=9393719; [NCBI, ExPASy, EBI, Israel, Japan]
Dworkin J., Shedd O.L., Blaser M.J.;
 "Nested DNA inversion of *Campylobacter fetus* S-layer genes is *recA* dependent."
J. Bacteriol. 179:7523-7529(1997).

Comments

- FUNCTION:** CAN CATALYZE THE HYDROLYSIS OF ATP IN THE PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC CLEAVAGE.

- **SUBCELLULAR LOCATION:** Cytoplasmic (*By similarity*).
- **SIMILARITY:** BELONGS TO THE RECA FAMILY.

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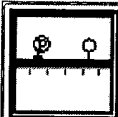
Cross-references

EMBL	AF020677; [EMBL / GenBank / DDBJ] AAB86923.1; -. [CoDingSequence]
HSSP	P26345; 1G19. [HSSP ENTRY / PDB]
HAMAP	MF_00268; -; 1.
InterPro	IPR003593; AAA_ATPase. IPR001553; RecA. Graphical view of domain structure.
Pfam	PF00154; recA; 1.
PRINTS	PR00142; RECA.
ProDom	PD000229; RecA; 1. [Domain structure / List of seq. sharing at least 1 domain] .
SMART	SM00382; AAA; 1.
PROSITE	PS00321; RECA_1; 1. PS50162; RECA_2; 1. PS50163; RECA_3; 1.
BLOCKS	O30884.
ProtoNet	O30884.
ProtoMap	O30884.
PRESAGE	O30884.
DIP	O30884.
ModBase	O30884.
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Keywords

DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.

Features



Feature table viewer

Key	From	To	Length	Description
NP_BIND	65	72	8	ATP (BY SIMILARITY) .

Sequence information

Length: 345 AA	Molecular weight: 37209 Da	CRC64: FOAA05048DD4B220 [This is a checksum on the sequence]
--------------------------	--------------------------------------	--

10	20	30	40	50	60
MDDNKKKS	LALDKQIDKAF	GKGTVLR	LGDK	KEIEPID	SIS
70	80	90	100	110	120
VEIYGPESSG	KTTTLTLHLIA	ESQKVG	GVCA	FVDAEH	ALDV
130	140	150	160	170	180
GEQALDIVET	LARSGAVDLI	VIDSVA	ALTP	KSEIEG	DMGD
190	200	210	220	230	240
VHKMGTTVVF	INQIRMKIGA	MGYGT	PETTT	GGNALK	FYAS
250	260	270	280	290	300
RVKVKVVKNK	VAPPPRQAEF	DIMFG	EGISK	EGEIID	YGVK
310	320	330	340		
GRENSKAFLK	ENKAIAD	EIT	EKIRAN	MGDS	IMSGAVDEEE
					MEGDE

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General information about the entry

Entry name	RECA <u>CAMJE</u>
Primary accession number	P42440
Secondary accession number	Q9PM04
Entered in Swiss-Prot in	Release 32, <u>November 1995</u>
Sequence was last modified in	Release 40, October 2001
Annotations were last modified in	Release 41, February 2003
Name and origin of the protein	
Protein name	RecA protein
Synonym	Recombinase A
Gene name	RECA or <u>CJ1673C</u>
From	<u>Campylobacter jejuni</u> [TaxID: <u>197</u>]
Taxonomy	<u>Bacteria</u> ; <u>Proteobacteria</u> ; <u>Epsilonproteobacteria</u> ; <u>Campylobacterales</u> ; <u>Campylobacteraceae</u> ; <u>Campylobacter</u> .

References

[1] SEQUENCE FROM NUCLEIC ACID.**STRAIN=**ATCC 55026 / 81-176;**MEDLINE=**94131574; **PubMed=**8300203; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]Guerry P., Pope P.M., Burr D.H., Leifer J., Joseph S.W., Bourgeois A.L.;"Development and characterization of *recA* mutants of *Campylobacter jejuni* for inclusion in attenuated vaccines.";*Infect. Immun.* 62:426-432(1994).**[2] SEQUENCE FROM NUCLEIC ACID.****STRAIN=**NCTC 11168;**MEDLINE=**20150912; **PubMed=**10688204; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C., Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M., Whitehead S., Barrell B.G.;"The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hypervariable sequences.";*Nature* 403:665-668(2000).**Comments**

- **FUNCTION:** CAN CATALYZE THE HYDROLYSIS OF ATP IN THE PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC CLEAVAGE.
- **SUBCELLULAR LOCATION:** Cytoplasmic (*By similarity*).
- **SIMILARITY:** BELONGS TO THE RECA FAMILY.

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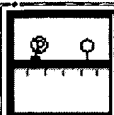
Cross-references

EMBL	U03121; AAA17793.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AL139079; [EMBL / GenBank / DDBJ] CAB73660.1; -. [CoDingSequence]
HSSP	P26345; 1G19. [HSSP ENTRY / PDB]
CMR	P42440; CJ1673C.
HAMAP	MF_00268; -: 1.
InterPro	IPR003593; AAA_ATPase. IPR001553; RecA. Graphical view of domain structure.
Pfam	PF00154; recA; 1.
PRINTS	PR00142; RECA.
ProDom	PD000229; RecA; 1. [Domain structure / List of seq. sharing at least 1 domain] .
SMART	SM00382; AAA; 1.
PROSITE	PS00321; RECA_1; 1. PS50162; RECA_2; 1. PS50163; RECA_3; 1.
BLOCKS	P42440.
ProtoNet	P42440.
ProtoMap	P42440.
PRESAGE	P42440.
DIP	P42440.
ModBase	P42440.
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Keywords

[DNA damage](#); [DNA recombination](#); [SOS response](#); [ATP-binding](#);
[DNA-binding](#); [Complete proteome](#).

Features



Feature table viewer

Key	From	To	Length	Description
NP_BIND	65	72	8	ATP (BY SIMILARITY) .
CONFLICT	217	217		F -> I (IN REF. 1) .

Sequence information

Length: 343 AA Molecular weight: 37049 Da CRC64: B5E7FE7FAF424598 [This is a checksum on the sequence]


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MDDNKRKSLD	AALKSLDKTF	GKGTILRLGD	KEVEQIDSIG	TGSVGLDLAL	GIGGVPKGRI
70	80	90	100	110	120
IEIYGPESSG	KTTLTLLHIIA	ECQKAGGVCA	FIDAEHALDV	KYAKNLGVNT	DDLVSQPDF
130	140	150	160	170	180
GEQALEIVET	IARSGAVDLI	VVDSVAALTP	KAEIEGDMGD	QHVGLQARLM	SQALRKLTGI
190	200	210	220	230	240
VHKMNTTVIF	INQIRMKIGA	MGYGTPETTT	GGNALKFYAS	VRLDVRKVAT	LKQNEEPIGN
250	260	270	280	290	300
RVKVKVVKNK	VAPPFRQAEF	DVMFGEGLSR	EGELIDYGVK	LDIVDKSGAW	FSYKDKKLQ
310	320	330	340		
GRENSKAFLK	ENPEIADEIT	KAIQNSMGIE	GMISGSEDDE	GEE	

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